1 SEQUENCE LISTING

<110> EVANS, RONALD M. <120> Novel steroid-activated nuclear receptors and uses therefor <130> SALK2270-2 <140> 09/458,366 <141> 1999-12-09 <150> 09/227,718 <151> 1999-01-08 <160> 09/005,286 <161> 1998-01-09 <170> 48 <190> PatentIn Ver. 2.1 <210> 1 <211> 2068 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (583)..(1884) <220> <221> modified_base <222> (1263) <223> a, c, t, or g <400> 1 ggcacgagga gatctaggtt caaattaatg ttgcccctag tggtaaagga cagagaccct 60 cagactgatg aaatgegete agaattactt agacaaageg gatatttgee actetettee 120 cetttteetg tgtttttgta gtgaagagae etgaaagaaa aaagtaggga gaacataatg 180 agaacaaata cggtaatete tteatttget agtteaagtg etggaettgg gaettaggag 240 gggcaatgga gccgcttagt gcctacatct gacttggact gaaatatagg tgagagacaa 300 gattgtctca tatccgggga aatcataacc tatgactagg acgggaagag gaagcactgc 360 ctttacttca gtgggaatet cggcctcage ctgcaageca agtgttcaca gtgagaaaag 420 caagagaata agetaataet eetgteetga acaaggeage ggeteettgg taaagetaet 480 cettgatega teetttgeac eggattgtte aaagtggace eeaggggaga agteggagea 540 aagaacttac caccaagcag tccaagaggo ccagaagcaa ac ctg gag gtg aga Met Glu Val Arg

ccc aaa gaa age tgg aac cat get gae ttt gta cae tgt gag gae aca 642
Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His Cys Glu Asp Thr

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5			10			15			20	
			aag Lys							690
			cgt Arg							738
			tgt Cys							786
			cgg Arg							834
			acc Thr 90							882
			ggc Gly							930
			cgg Arg							978
			ctg Leu							1026
			ctg Leu							1074
			aag Lys 170							1122
			gag Glu							1170
			gtc Val							1218
			gag Glu							1266
			ааа ҍуз							1314

gac atg tca acc tac atg ttc aaa ggc atc atc agc ttt gcc aaa gtc 1362 Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val

									3							
245					250					255					260	
atc Ile	tcc Ser	tac Tyr	ttc Phe	agg Arg 265	gac Asp	ttg Leu	ccc Pro	atc Ile	gag Glu 270	gac Asp	cag Gln	atc Ile	tcc Ser	ctg Leu 275	ctg Leu	1410
														gtg Val		1458
														tgc Cys	ttg Leu	1506
														atg Met		1554
														gag Glu		1602
														ggt Gly 355		1650
														att Ile		1698
														agg Arg		1746
										Glu				atc Ile		1794
	Gln	His	Thr	Gln		Leu	Leu	Arg	Ile	Gln	Asp	Ile		ccc Pro		1842
					cag Gln									tga		1887
gtgg	gctgt	cc t	tggg	gtgad	a co	tccç	jagaç	gta	gtta	agac	ccag	gagco	et d	etgag	jtegee	1947
acto	ccgg	igc o	aaga	acaga	it go	jacac	tgc	aag	jago	gac	aatç	jecet	gc t	ggcc	tgtct	2007
ccct	aggg	gaa t	tcct	gcta	at ga	cago	etggo	tag	gcatt	cct	cago	gaagg	gac a	tggg	gtgcc	2067
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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala 35 40 45

Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe 50 60

Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg 65 70 75 80

Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala 85 90 95

Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile 100 105 110

Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys 115 120 125

Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr 130 140

Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys 145 150 155 160

Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly 165 170 175

Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser 180 185 190

Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser 195 200 205

Leu Lys Val Ser Leu Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn 210 215 220

Tyr Lys Pro Pro Ala Asp Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu 225 230 235 240

Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser 245 250 255

Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln

260

265

270

Tle Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe 275 280 285

Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu 290 295 300

Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu 305 310 315

Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His 325 330 335

Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp 340 345 350

Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln 355 360 365

Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro 370 375 380

Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu 385 390 395 400

Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
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Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr 420. 425 430

Gly Ser

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~22A~

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 rCYP3A1

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25

<210> 4

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<212> DNA

<213> Artificial Sequence

<2205

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	rbCYP2C1	
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<210> 9

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	rCYP2A2	
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graci	ggttc aactggaggt cagtatg	27
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	1019200	
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agccc	acce agegggger cageete	21
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	hCYP2E1	
	HC172H1	
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gagato	gttc aaggaagggt cattaac	27
J- J- 73	.g	- '
<210>	12	
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	Artificial Sequence	
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<220> <223> <400>	Description of Artificial Sequence: Direct repeat with spacer of 0 nucleotides	
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<220>
<223> Description of Artificial Sequence: Dir ct repeat
      with spacer of 5 nucleotides
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                                                                    31
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                                                                    33
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      with spacer of 7 nucleotides
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                                                                    33
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      with spacer of 10 nucleotides
catagicagg tcatatatat ataaggicag atcaac
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<210> 21
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<212> DNA
<213> Artificial Sequence
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<210><211><212><212>	19	
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	Description of Artificial Sequence: Inverted repeat response element with spacer of 4 nucleotides	
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 <223> Description of Artificial Sequence: Inverted
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                                                                     23
<210> 31
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<210> 38
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Arg Gly Lys Thr Cys Ala
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